geneplast.data

March 25, 2026

`make.cogdata` *Parse orthogroups tabular output from OrthoFinder into a ‘cogdata‘ data frame for geneplast*

Description

Parse orthogroups tabular output from OrthoFinder into a ‘cogdata‘ data frame for geneplast

Usage

```
make.cogdata(file)
```

Arguments

`file`	OrthoFinder orthogroups tabular file

Value

cogdata data frame

Author(s)

Leonardo RS Campos

`make.phyloTree` *Build a ‘phyloTree‘ object for geneplast*

Description

This function has two optional arguments that define its behavior depending on which one is provided. Given a list of species’ NCBI Taxonomy IDs, ‘make.phyloTree()‘ builds a phylogenetic tree by merging the TimeTree and NCBI Taxonomy databases. If given a newick file, it simply forwards the argument to [treeio::read.newick()].

Usage

```
make.phyloTree(sspids = NULL, newick = NULL, verbose = TRUE)
```

Arguments

`sspids`	a vector or data frame containing NCBI Taxon IDs from the species of interest.
`newick`	a phylogenetic tree in Newick format.
`verbose`	a logical value specifying whether or not to display detailed messages.

Value

An object of class "phylo".

Author(s)

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